

NEB 1233

-1391	-1381	-1371	-1361	-1351	-1341	-1331	-1321
*	*	*	*	*	*	*	*
AGCGGATAC AATTTCACAC AGGAACAGC TATGACCATG ATTACGCCAA GGTGGTACC GAGCTCGGTT CCACAGTAA							
pCR2.1				-BamHI-			
Lac promoter →							
-1311	-1301	-1291	-1281	-1271	-1261	-1251	-1241
*	*	*	*	*	*	*	*
CGGCCGCCAG TGTGCTGGAA TTGGCTTAC TATAGGSCAC GCGTGGTCCA CCGCCCGGCG TGGTAACCTT AAGAGAATT							
pCR2.1				-SmaI-			
GenomeWalker Adaptor →							
cmAC01 →							
-1231	-1221	-1211	-1201	-1191	-1181	-1171	-1161
*	*	*	*	*	*	*	*
GGTAAATTC CTAGAGAGAA TTGTAATTAA TATAGAGAA TGATTTTAAT TCTAATGTG TATCACTTT CGATAAAGTT							
cmAC01 Genomic DNA →							
-1151	-1141	-1131	-1121	-1111	-1101	-1091	-1081
*	*	*	*	*	*	*	*
AAATAAGTG TGTAGACGA CCATCATCT TAATCACTTT GTACTTATCA AATTGTATC TGAGATTAA GTCAAAATC							
cmAC01 Genomic DNA →							
-1071	-1061	-1051	-1041	-1031	-1021	-1011	-1001
*	*	*	*	*	*	*	*
ACACTAAAC AATGAAATG TATGGACAA TCACAATGGA AAATAAGTAT GATGATATCC ATCACTTTC AAGTCTAAC							
cmAC01 Genomic DNA →							
-991	-981	-971	-961	-951	-941	-931	-921
*	*	*	*	*	*	*	*
CTAGGATATG TTTTGAATA TTGAGATT ATTAATTTAT TCTTTTATCC GTTGACAGTT TMTTTTGT TTAAGATGT							
cmAC01 Genomic DNA →							
-911	-901	-891	-881	-871	-861	-851	-841
*	*	*	*	*	*	*	*
ATGTAAGAAA CGAGAAATA TGTGATTAAA CCAAGATGCG ATCAAAATA GAGCTAGATC CTAAAGATAT ATAAAGAT							
cmAC01 Genomic DNA →							
-831	-821	-811	-801	-791	-781	-771	-761
*	*	*	*	*	*	*	*
GATCAACAC GATCAAAAG TTTCITTTG ATGATAATTA TCTTAAGAAC TTCAAGGTTA ATTAGATCT CTAAATTAA							
cmAC01 Genomic DNA →							
-751	-741	-731	-721	-711	-701	-691	-681
*	*	*	*	*	*	*	*
AAATTTCAAT GATATGCGT CCGTGAACAA GAAAAACAT AAAGAACCA TGGTTGTCCT AATTTTGTGA GTAATTAAGC							
cmAC01 Genomic DNA →							
-671	-661	-651	-641	-631	-621	-611	-601
*	*	*	*	*	*	*	*
GTATCTAAG ACACAAGTAA GAATGAAGTT ACCACATGTT AATCTAGATT CCAAACTTG AGCTGAGAG CAOSTTACGA							
cmAC01 Genomic DNA →							

**Fig. 1A**



-1289	-1279	-1269	-1259	-1249	-1239	-1229	-1219
*	*	*	*	*	*	*	*
AGGAACACG TAATACGCTG ATTACGCCAA GCTTAAGACA AMTGTGAAA ATTCTAGAG AGAATTGTAA TTAATATAGG							
HindIII							
pUC19				cmAC01 Genomic DNA			
-1209	-1199	-1189	-1179	-1169	-1159	-1149	-1139
*	*	*	*	*	*	*	*
AGAATGATTT TAATCTAAT GTTGATCCA TTGTGATA AGTTAAATAA AGTGTGAG AGGACCATCA TTCTTAATCC							
cmAC01 Genomic DNA							
-1129	-1119	-1109	-1099	-1089	-1079	-1069	-1059
*	*	*	*	*	*	*	*
ATTGTACTTT ATCAAATTG TATCTGAGAT TTAAGTCAA ATTCACACTA AAACAATCGA AATGTATGCG ACAATCACAA							
cmAC01 Genomic DNA							
-1049	-1039	-1029	-1019	-1009	-999	-989	-979
*	*	*	*	*	*	*	*
TGGAATATC GTATGATGTA TTCCATCACC TTTCAGTTC TAACCTAGGA TATGTTTTGG AATATTGTAG ATTATATAAA							
cmAC01 Genomic DNA							
-969	-959	-949	-939	-929	-919	-909	-899
*	*	*	*	*	*	*	*
TTATCTTTT ATCCGTTGAC AGTTTATTTT TTGTTTAAAG ATGTATGATA GAACGACGA AATATGTGAT TAAACCAAGA							
cmAC01 Genomic DNA							
-889	-879	-869	-859	-849	-839	-829	-819
*	*	*	*	*	*	*	*
TCCATACAA ATTAAGCTTA GATCTTAAG ATATATAAAA GTATGATCAA CAACTGACAA AACGTTCTTT TTGATGATA							
cmAC01 Genomic DNA							
-809	-799	-789	-779	-769	-759	-749	-739
*	*	*	*	*	*	*	*
ATTATCTTAA GACCTCAAG GTTAATTTAG ATCTCTTAAT TAAAAATTT CATAGATAT GCATCCGTGA ACAAGAAAAA							
cmAC01 Genomic DNA							
-729	-719	-709	-699	-689	-679	-669	-659
*	*	*	*	*	*	*	*
ACATTAAGAA CCCATGGTG TCTAATTTT TGTAGTAAAT AAGGTGAGTT CAAGACACAA GTAAGAATGA CGTTACCA							
cmAC01 Genomic DNA							
-649	-639	-629	-619	-609	-599	-589	-579
*	*	*	*	*	*	*	*
TGTTAATCTA GATTCACAAA CTTGAGCTG AGACCAAGTT ACAGAAATAA TCTACGAAAA CGAGTAAGTC GTCTAAGTTC							
cmAC01 Genomic DNA							
-569	-559	-549	-539	-529	-519	-509	-499
*	*	*	*	*	*	*	*
GTTTGTGTTT ATTGTACAG TAAGATCTC GTATTGAAAG AAGACGAAAA ATGGAAAAAA GTTAAAGAAG TAAGGAGGTG							
cmAC01 Genomic DNA							

**Fig. 2A**

```

-489      -479      -469      -459      -449      -439      -429      -419
  *        *        *        *        *        *        *        *
GGTGAGTCCA AAGGAAACAT ACCAAATTCA TGCAAGAAGCT ATGAGATTCA GAAATTAGAG GAAAGTGTG GAAATCATGT
cm#C01 Genomic DNA
>

-409      -399      -389      -379      -369      -359      -349      -339
  *        *        *        *        *        *        *        *
AACTAAATTT AAAATACATA TAGGTACTAT TTCTTTCTCT TTCTTATTTG AASRAAGAGA NNAGGGGGG AATTAGTGTAT
cm#C01 Genomic DNA
>

-329      -319      -309      -299      -289      -279      -269      -259
  *        *        *        *        *        *        *        *
ATGGCATTGG CAGACATPAA AATAATAAAG TTAAATCATA TTGGGTCCCA AACTCACCAA AGAGGAAATT CAGTGTGTGA
cm#C01 Genomic DNA
>

-249      -239      -229      -219      -209      -199      -189      -179
  *        *        *        *        *        *        *        *
TAAAGCCATT TAGCCAAAGC CAAAGOCAAA GCGACTCTCT CTCTTTCCCA CATACATGCA TGAAATTTCG TGGGCCCAT
cm#C01 Genomic DNA
>

-169      -159      -149      -139      -129      -119      -109      -99
  *        *        *        *        *        *        *        *
CTTTTATCA TCACATTTTT AATAATTFTA TCTTCTCTT CTCTCTCTT TCTTCTCTT TCTTCTCTT CTCTCTCTT
cm#C01 Genomic DNA
>

-89      -79      -69      -59      -49      -39      -29      -19
  *        *        *        *        *        *        *        *
TCTTTTCTTT ATCAATTTC TTCCACTTT CCAATCTTAA ATAAATTTCG CTATAAATAC CCTTCATTA TAACTGTATC
cm#C01 Genomic DNA
>

                                TATA box
                                |
                                -39
                                *
transcriptional start site in Tomato E4
|
-9      2      12      translational start site
  *      *      *      |
CAACACACCC AGGATCCATT AATTAGAGATT GAGCC ATGG
          BamHI
__cm#C01__      __Tom E4 5'UTR__

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**Fig. 2B**

NEB 1233

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-1669      -1659      -1649      -1639      -1629      -1619      -1609      -1599
  *          *          *          *          *          *          *          *
AGCGGATAAC AATTTCACAC AGGAACACG TATGAACATG ATTACGCCAA GCTTGTAACC GAGCTGGGAT CCACTAGTAA
                                     HindIII      -BamHI-
____Lac promoter____>
____PCR2.1____>

-1589      -1579      -1569      -1559      -1549      -1539      -1529      -1519
  *          *          *          *          *          *          *          *
CGCGCGCCAG TGTGCTGGAA TTGCGCTGTG AATACGACTC ACTATAGGAC ACGCGTGGTC CAGCGCCCGG GCCTGTAACT
____PCR2.1____>
____GenomeWalker Adaptor____>

-1509      -1499      -1489      -1479      -1469      -1459      -1449      -1439
  *          *          *          *          *          *          *          *
AGGAGCTAAA GGACGAAGTC AACATATATA AAATTACTTC AAGATAATTA AAATTAAAAA TACTTTATAT TTTATGGGCT
____MEL7 promoter____>

-1429      -1419      -1409      -1399      -1389      -1379      -1369      -1359
  *          *          *          *          *          *          *          *
TACATCTTCC TTCTCTCTTC TCTTTTCTTC TCGTCGGATT TCTGCCATC TATTCTTCTT TTACTCTCTA TTTTCTCTT
____MEL7 promoter____>

-1349      -1339      -1329      -1319      -1309      -1299      -1289      -1279
  *          *          *          *          *          *          *          *
TACATGTGTT AGATTGGGAT AACCAATCT GATTCTTTC TATCGTCTT CTCTCTTTC TCCTTTTTTT TCGCTGGA
____MEL7 promoter____>

-1269      -1259      -1249      -1239      -1229      -1219      -1209      -1199
  *          *          *          *          *          *          *          *
TTCTCTCCA TTGCTATGCG TTTTCTCTTC TTTTTTTTTT TACATGTTAA CCAATCTTAA AAGATGTTAT ATAAAGATC
____MEL7 promoter____>

-1189      -1179      -1169      -1159      -1149      -1139      -1129      -1119
  *          *          *          *          *          *          *          *
TTCAAAAAAA AAAATTGTTT AGATTGGAGT AGCCAAATTT AACCAATGCG GTAAAAAAAA TAAAGCTGTC TAGACAATC
____MEL7 promoter____>

-1109      -1099      -1089      -1079      -1069      -1059      -1049      -1039
  *          *          *          *          *          *          *          *
TAAACGATCG TGCACAAAAA GATTTAAAAA AATCGTTTAG TCAATCTTAA ACAATTGTAT AACCAATTA AAGATAGAA
____MEL7 promoter____>

-1029      -1019      -1009      -999      -989      -979      -969      -959
  *          *          *          *          *          *          *          *
TTGAAATAT AAATGGTTA GATTGGCTA TCCAATTTA AATGAACAAA TCTAAAGAT CGTATACAA ATCTAAAGA
____MEL7 promoter____>

```

**Fig. 3A**

-949	-939	-929	-919	-909	-899	-889	-879
*	*	*	*	*	*	*	*
TGGKATACCA AATCTAAATG ATCATGTACC AAATATATTA TGCACATGT TGGCAGGGTG GTTGAAGGAA CATTTTGTAT							
MEL7 promoter							
-869	-859	-849	-839	-829	-819	-809	-799
*	*	*	*	*	*	*	*
ATTTTCTATT ATGGGTTTGT AGAATTTTIT CATTTTGGAA ATTGTTCIAT ACAATATAAA TATTAATATT TTACCACTTC							
MEL7 promoter							
-789	-779	-769	-759	-749	-739	-729	-719
*	*	*	*	*	*	*	*
GTTATATTTT CGAAAAGACC OCTTAATAA ATTTGAATTC CATTATATTA AAATTTTTTC CCAAAAAAG TGAATATGT							
MEL7 promoter							
-709	-699	-689	-679	-669	-659	-649	-639
*	*	*	*	*	*	*	*
CCTATTAATA ATTTGATTC CATTATAGAA CAATTTTCCA AATGTAACAA ACATTTGAAA TTCTCGATAT AGAAAACATT							
MEL7 promoter							
-629	-619	-609	-599	-589	-579	-569	-559
*	*	*	*	*	*	*	*
TACTTATTTT GAATTTGGAC ATATTCACAA GTTTATTCOA AACGTAACIT TGAAGGAAA GTTGTATGAG ATTACATCCA							
MEL7 promoter							
-549	-539	-529	-519	-509	-499	-489	-479
*	*	*	*	*	*	*	*
TATTTTGTGT TTTCATATGG AATTTTCATGG AAAATTAATA TGCACACAAA ATGATGTATG AGATTAACCC AAAGTTTATC							
MEL7 promoter							
-469	-459	-449	-439	-429	-419	-409	-399
*	*	*	*	*	*	*	*
GTTATATGAT TCTTTTATTA AAAAACCAAC AAAATTTTAA AACTGTTTGG CAATAGACCA ATATAGTTAA TCCATCGTGG							
MEL7 promoter							
-389	-379	-369	-359	-349	-339	-329	-319
*	*	*	*	*	*	*	*
TCTATTTGAT ATAAATTTGA ATATTTTGT ATATTTAATA AATATTTTGA TTTATTTTGA TATATTTTGA TTTAGATAAC							
MEL7 promoter							
-309	-299	-289	-279	-269	-259	-249	-239
*	*	*	*	*	*	*	*
AAATATAGA TTTAATATT ATTTTATATC TTAATATATA CATTTGTATA TTTTTCIAT TTTAGACAT TTCTCTATT							
MEL7 promoter							
-229	-219	-209	-199	-189	-179	-169	-159
*	*	*	*	*	*	*	*
TTTATATTAAC ATTTTATATA CTAAATGAT TGCACACAC TAATATATT TTTATCCAA GAAATATATG CTATATAATA							
MEL7 promoter							

**Fig. 3B**

```

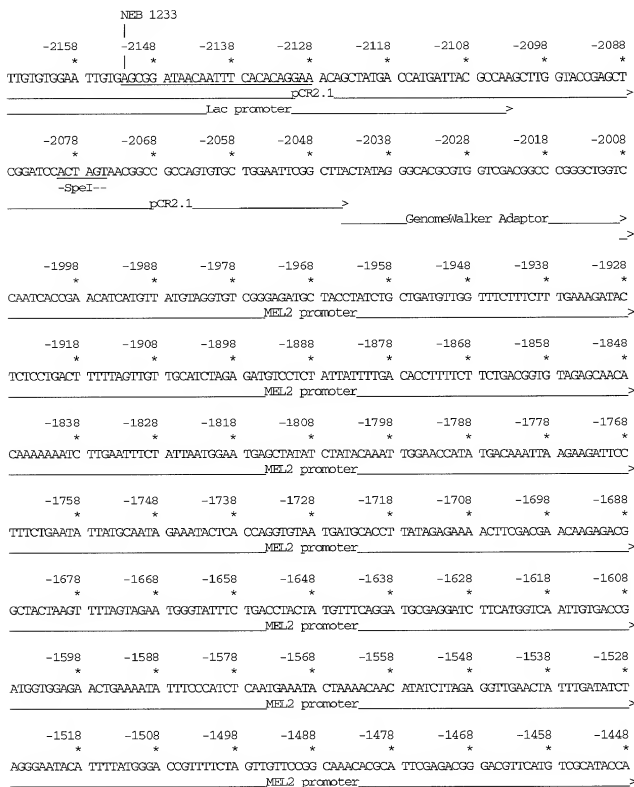
-149      -139      -129      -119      -109      -99      -89      -79
  *        *        *        *        *        *        *        *
TGGGTCMCT TTAICACCTT CATGATAATT ATGAAAAATA AAATAAAATT TAATTATATA ATTCATTTCA TCCTAATOGIA
MEL7 promoter>

                                TATA box
-69      -59      -49      -39      -29      -19      -9      2
  *        *        *        *        *        *        *        *
CAAGCTAGAT ATTACTATAT CAACAACITT GTGTAATAAA AGGGCAAGAA ATTAAGCATT ATCGTGTGAG CCACITTTTC
MEL7 promoter>

                                Mel7 translational start site
                                <cmDruNcoSt
                                |
12      22      32      42      52
  *        *        *        *        *
TATATCTAGA GATAGAAGGT TTAAMTCAT GTCTCATTT GGAAGGCTTG TGAGT
TTCCA AATTTTgGTA CcGAGAgTAA CcTTTCG
-NcoI-
MEL7 promoter>
                                MEL7 cds>

```

**Fig. 3C**



**Fig. 4A**



-1438	-1428	-1418	-1408	-1398	-1388	-1378	-1368
*	*	*	*	*	*	*	*
CGGAGGATCC	GCATGTAAAC	TATCAAGCA	ATACTTCAC	CCCTTTTGTC	TTCCTTATAT	ATATATTTT	TACTTACTAA
MEL2 promoter							
-1358	-1348	-1338	-1328	-1318	-1308	-1298	-1288
*	*	*	*	*	*	*	*
GATAGTTTTC	AAATTTGTG	TAGAATCGAA	TGCTGGAAC	TCAGTCTCAG	CTTACCTCAG	TGGGTACTTA	GCCACTCTCT
MEL2 promoter							
-1278	-1268	-1258	-1248	-1238	-1228	-1218	-1208
*	*	*	*	*	*	*	*
GCGGACAAGA	TATGCGAGAT	GCGTTGGAT	AGAAGATTGG	ACTACTCAA	AGGCTTGGT	TGGGGACTTA	AGTCTAGGCG
MEL2 promoter							
-1198	-1188	-1178	-1168	-1158	-1148	-1138	-1128
*	*	*	*	*	*	*	*
CCCAAGACG	GCCAGTGTGA	GTAGTTCCAC	GACTCATGT	TGTGTAGTCA	CGGTAGAGCT	CCATTTATGG	ACTAAGCTTG
MEL2 promoter							
-1118	-1108	-1098	-1088	-1078	-1068	-1058	-1048
*	*	*	*	*	*	*	*
ATCAAGCTGT	GCAACGGATT	GAAGACAAA	CAAGAAATCA	CGATCGGTTA	GCTTCAAAAG	TGGAATGAAT	GTGAAGTTC
MEL2 promoter							
-1038	-1028	-1018	-1008	-998	-988	-978	-968
*	*	*	*	*	*	*	*
ATAGAAGACA	TGAGTCGGCG	ACAGTAAGGA	CCACACATT	ATCTTTAGCT	TTGCGATACG	TATANNATTT	TCCATTTATTC
MEL2 promoter							
-958	-948	-938	-928	-918	-908	-898	-888
*	*	*	*	*	*	*	*
TTAAGTTTTT	GAATTACAGT	ATTCAGTGAT	GAATAGCATA	TATAGTATAC	AAAGTAGCC	ACTTTTGAT	AATTGTAGGA
MEL2 promoter							
-878	-868	-858	-848	-838	-828	-818	-808
*	*	*	*	*	*	*	*
OCTGTGTGT	AGAATGGCAT	ATGAGGCTCG	TTAAAAGACA	TACGATTTTC	TTTGTGCTTT	TTTTAAGGAG	GAATTTTTTT
MEL2 promoter							
-798	-788	-778	-768	-758	-748	-738	-728
*	*	*	*	*	*	*	*
TATTGTATTT	ATGAACITTA	TTACATTTCT	TGAATTTCT	TGATATATGA	AGATTTAAT	TTTTGTGAA	TTTTTGTGTT
MEL2 promoter							
-718	-708	-698	-688	-678	-668	-658	-648
*	*	*	*	*	*	*	*
TATTTTGTA	TTTACTAAT	TATTTTAAT	TTTCTTAAT	TGAATCGATA	ACGAATGCAA	ATATTTTACG	AAAAAACCTT
MEL2 promoter							

**Fig. 4B**

```

-638      -628      -618      -608      -598      -588      -578      -568
  *        *        *        *        *        *        *        *
ATAGGAAGAT ATTTCAGAAA AATAAAAAAT TACATATTTA AAATATTTTT CGAGCGATTA CATATGTGGA AAATATGGTG
MEL2 promoter_>

-558      -548      -538      -528      -518      -508      -498      -488
  *        *        *        *        *        *        *        *
CAAACATCAG ATGGGGGATG GTTATTACCG ACGCATGAAT GACACCGAAT ATATAAAGT AAGGAATAGT TAITTOGTAC
MEL2 promoter_>

-478      -468      -458      -448      -438      -428      -418      -408
  *        *        *        *        *        *        *        *
GCATAACTGC TGTCGGAACT GTGGAGTTA GTTCTCGACA TTATTAACAC TTACGTGAC GTTTTTATGC ATGCGGAGTC
MEL2 promoter_>

-398      -388      -378      -368      -358      -348      -338      -328
  *        *        *        *        *        *        *        *
GCTOCATTC TTGTAGTGAA GAAATTTTGC CTATTAATGTC GGTTTAAAC CGACATTAAG GCGCAAAATT CTCTAGTGC
MEL2 promoter_>
Imperfect inverted repeat

-318      -308      -298      -288      -278      -268      -258      -248
  *        *        *        *        *        *        *        *
ATATCAATA TMCAGAGT CAATTCAGAA AATTACATTT CTCTAGAAAT TCGTGTGAA CAATTGTAT AAAGGTTTAA
MEL2 promoter_>

-238      -228      -218      -208      -198      -188      -178      -168
  *        *        *        *        *        *        *        *
AGTGAATTGA AAATTTCAG ACGTAATGG ATTACGCGAG AAAATATATTT TAATCAOAT TCAGAAAGTTA TTACAAATGA
MEL2 promoter_>

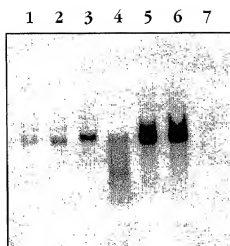
-158      -148      -138      -128      -118      -108      -98      -88
  *        *        *        *        *        *        *        *
AAAAATAGGA AGATAAGATT TCAAAATTAC GTAAATTACT TCTACGTTTC TTCTCTTCC CTTTAGTAC TTCACATCA
MEL2 promoter_>

TATA box
| -78      -68      -58      -48      -38      -28      -18      -8
  *        *        *        *        *        *        *        *
TCTTTATATA CGTTCATCC CTTCACATTC TCATACAGAA TTCTCTTTCA ATATCAACTC TCCTCTCTTA ACTCACCCCT
MEL2 promoter_>

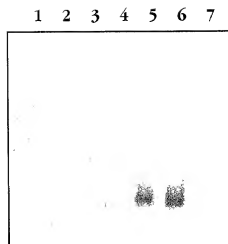
MEL2 translational start site
| <MEL2_Nco_R
1 3      13
* *      *
TTTTCAGATG GAAACATGTC AATC
AAGgggtAC CTTTGTTACG TTTC
-NcoI--
pro_
MEL2 cds_>

```

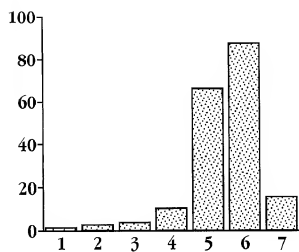
**Fig. 4C**



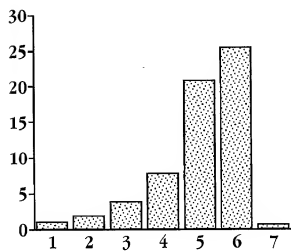
**Fig. 5A**



**Fig. 5C**



**Fig. 5B**



**Fig. 5D**

-968        -958        -948        -938        -928        -918        -908        -898  
 \*           \*           \*           \*           \*           \*           \*           \*  
 TGGAAITGIG AGCGGATPAC AATTTCACAC AGGAACAGC TATGACCATG ATTAGGCCAA GCTIGGTAC GAGCTCGGAT  
BamHI>  
 \_\_\_\_\_pCR2.1\_\_\_\_\_>  
 \_\_\_\_\_Lac promoter\_\_\_\_\_>  
 -888        -878        -868        -858        -848        -838        -828        -818  
 \*           \*           \*           \*           \*           \*           \*           \*  
 CCACTAGTAA CGGCGGCAG TGTGCTGAA TTGCGCTAC TATAGGGCAC GGTGTGTGCA CGGCGGCGC TGTGAAATTT  
 \_\_\_\_\_pCR2.1\_\_\_\_\_>  
 \_\_\_\_\_GenomeWalker Adaptor\_\_\_\_\_>  
 \_\_\_\_\_6E\_\_\_\_\_>  
 -808        -798        -788        -778        -768        -758        -748        -738  
 \*           \*           \*           \*           \*           \*           \*           \*  
 TGAAGAATA GGAGATATTT TTACATATA AGAGATATTT TTTATAATGT AACATTTTTT TTAGTAGACG GTTAGAGTGA  
 \_\_\_\_\_6E melon genomic DNA\_\_\_\_\_>  
 -728        -718        -708        -698        -688        -678        -668        -658  
 \*           \*           \*           \*           \*           \*           \*           \*  
 GTTAGGTTAA AGAAGGAAA ACTATAAAT AATTTTTAAT TATTAATATC ATAAACAATA CTTTGTATTC TATATTAATT  
 \_\_\_\_\_6E melon genomic DNA\_\_\_\_\_>  
 -648        -638        -628        -618        -608        -598        -588        -578  
 \*           \*           \*           \*           \*           \*           \*           \*  
 AAAATGACTA TTGAATTGTT AAGATGTAGG TATCTAAGGA CAAGAAGTCT CGAGTTCAAA TCTTCAAOCT CAAATATATC  
 \_\_\_\_\_6E melon genomic DNA\_\_\_\_\_>  
 -568        -558        -548        -538        -528        -518        -508        -498  
 \*           \*           \*           \*           \*           \*           \*           \*  
 TGCAAGATAG TAACTAATGA ATTATATTTG ACTAAATCAT GTAGCAAAAG AAAATCAAAAT TTATCATGTT AATATGGTC  
 \_\_\_\_\_6E melon genomic DNA\_\_\_\_\_>  
 -488        -478        -468        -458        -448        -438        -428        -418  
 \*           \*           \*           \*           \*           \*           \*           \*  
 AAGCGGAGC ATTACAACA ACAATTCATA TTTGTGGTIG ATAGTACTTG ACTAGAATTT AGAGAGTACT TGACTAGAT  
 \_\_\_\_\_6E melon genomic DNA\_\_\_\_\_>  
 -408        -398        -388        -378        -368        -358        -348        -338  
 \*           \*           \*           \*           \*           \*           \*           \*  
 AAAAATGGG GGACCCACTA CGAATTCAGC TTGCGTGTCT TAGCAATTAA GGTATCAOCT CTTAGTCTAT AGCTTGGTC  
 \_\_\_\_\_6E melon genomic DNA\_\_\_\_\_>

**Fig. 6A**

-328            -318            -308            -298            -288            -278            -268            -258  
 \*               \*               \*               \*               \*               \*               \*               \*  
 GCIGCATPAA ACGGTATTCT CACACTTTTC TTTCCTTTTT ACAGCACCCG TOCGGTATAT GGCTCCOCCA CTTTCTAOC  
 \_\_\_\_\_ 6E melon genomic DNA \_\_\_\_\_>

-248            -238            -228            -218            -208            -198            -188            -178  
 \*               \*               \*               \*               \*               \*               \*               \*  
 TCCCGAATC CAGGOCAGTT GCGAACATGC GAAGCAGCAA GTACATATTT GTCATTTTTC ATTACACAAA ATGACACGTC  
 \_\_\_\_\_ 6E melon genomic DNA \_\_\_\_\_>

box

TATA  
 -168            -158            -148            -138            -128            -118            -108            -98  
 \*               \*               \*               \*               \*               \*               \*               \*  
 GGTGTCTMT TATGTAATTA AGCTACAAAG CCAOGGTTAG TTTCGGAACC CCCACGATCC AGTACTTTAG TGTCCTCTMT  
 \_\_\_\_\_ 6E melon genomic DNA \_\_\_\_\_>

-88            -78            -68            -58            -48            -38            -28            -18  
 \*               \*               \*               \*               \*               \*               \*               \*  
 AAATCTTGA AGCAACGCTT TTACGGGAAT CAATCAITTA GGTATCCCAT TTTCATCTAT CAATTCACOC TTGAACCTGC  
 \_\_\_\_\_ 6E melon genomic DNA \_\_\_\_\_>

6E translational start site

|  
 <6E MelNcoP

-8            1 3  
 \*            \* \*

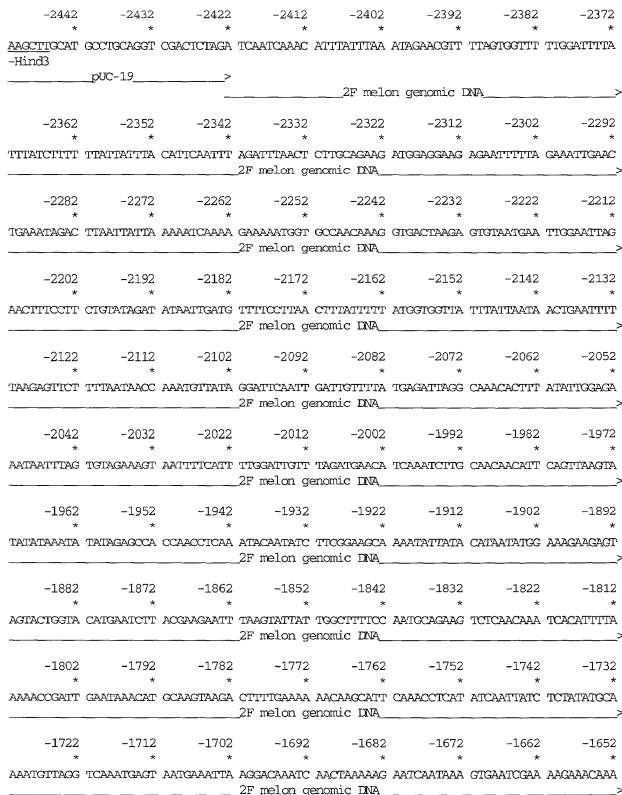
TTTTCCCGGC ACGSACT ATG GGC TC

AAAGGGGCGG aGCTGg TAC CGG A

--NcoI--

\_\_\_\_\_ 6E melon genomic DNA \_\_\_\_\_

**Fig. 6B**



**Fig. 7A**

-1642      -1632      -1622      -1612      -1602      -1592      -1582      -1572  
 \*           \*           \*           \*           \*           \*           \*           \*  
 TATCAATCAA ACCTAATGTA TACGTGATG ATGATGCAAT GGTGTTTGG ATATGGACAT TTGTATAAAC AACAAACCTC  
 2F melon genomic DNA

-1562      -1552      -1542      -1532      -1522      -1512      -1502      -1492  
 \*           \*           \*           \*           \*           \*           \*           \*  
 CACTCCAAAT CGAGAAGAGA GGCATTGAGT GACAGATTAG TGCCCTATTG AAGAGGGTAA GTCCAAAACA AACAAACAC  
 2F melon genomic DNA

-1482      -1472      -1462      -1452      -1442      -1432      -1422      -1412  
 \*           \*           \*           \*           \*           \*           \*           \*  
 AAAACATGTT GAAGAAATGT TATGAATAAA TGGCAGGGAA AGACATGGTT GTACATGTGG TGTGAGTTTT CTCTCTTCAA  
 2F melon genomic DNA

-1402      -1392      -1382      -1372      -1362      -1352      -1342      -1332  
 \*           \*           \*           \*           \*           \*           \*           \*  
 ATCTGTGATT AAATTGGATT ACGACCCAC AAGAGAAACA CIGTTTGGAA ACCATGACAG GGTCAACCCA TGGGTGAT  
 -NcoI-  
 2F melon genomic DNA

-1322      -1312      -1302      -1292      -1282      -1272      -1262      -1252  
 \*           \*           \*           \*           \*           \*           \*           \*  
 ATCAAGATTT TAATTAATTA AGCTCTATC CCGCGCATTC GTTTTTTTAT TCGATTCTTA TCTTATATTT TATATACGAA  
 2F melon genomic DNA

-1242      -1232      -1222      -1212      -1202      -1192      -1182      -1172  
 \*           \*           \*           \*           \*           \*           \*           \*  
 TAATTCCTGA GTTTGATTC AATTAGTTC GTCAATAGTA ATATTTTAAA CTATGTGTAAT ATATAAAAG TAAATGCGAA  
 2F melon genomic DNA

-1162      -1152      -1142      -1132      -1122      -1112      -1102      -1092  
 \*           \*           \*           \*           \*           \*           \*           \*  
 TGATCTAAT AGTATGACAT TTATATCACT CCTCTCTTGA GTAAAGTTTT TAAATGCGA AGGGAATGG AATACAGCT  
 2F melon genomic DNA

-1082      -1072      -1062      -1052      -1042      -1032      -1022      -1012  
 \*           \*           \*           \*           \*           \*           \*           \*  
 GTGATTTGGA GTTAATATTC CTATGACAG AGGTACTGT TTCTTACTTT ATATATATGG AGTATCTCT AATTTTTTCAA  
 2F melon genomic DNA

-1002      -992      -982      -972      -962      -952      -942      -932  
 \*           \*           \*           \*           \*           \*           \*           \*  
 CTCCTCACTT CCATTTATAC AAGCAAAACA TTCAATACCA TACATGCATC TTTTGTAGAA GAAAGAGAT TCTCTCTGG  
 2F melon genomic DNA

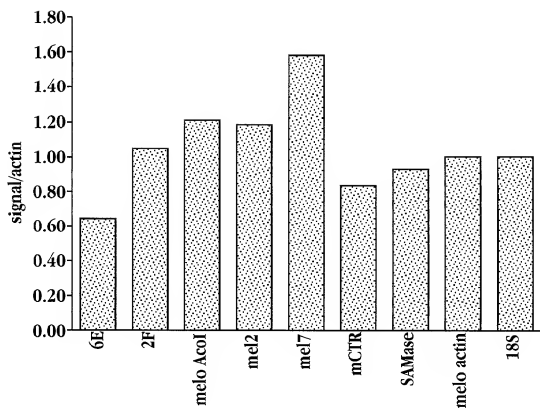
-922      -912      -902      -892      -882      -872      -862      -852  
 \*           \*           \*           \*           \*           \*           \*           \*  
 ACTTTTCTTT TCAATTCAC TATGCACCTT TGTATATTTA GTTTTATAT TTTTGTGTGT TCTTCCGTTT AATCAAGTTG  
 2F melon genomic DNA

**Fig. 7B**

-842	-832	-822	-812	-802	-792	-782	-772
*	*	*	*	*	*	*	*
TTGTAATCAA CTTTATGTAT TCAAACACAT AGATATTTTG TTTAATAGTA TCAGTATATA ATAGGSGTAG AATAACCTTT							
2F melon genomic DNA							
-762	-752	-742	-732	-722	-712	-702	-692
*	*	*	*	*	*	*	*
CAATATGTG TTTTAAAAA ATCAATACAC TTTAAAAAAT AAAATAIGTT TAATTAGTGT AIGTTTTTCT TTTAAGTGT							
2F melon genomic DNA							
-682	-672	-662	-652	-642	-632	-622	-612
*	*	*	*	*	*	*	*
TAAACACGA TAAAAAGTGC TTTAACACTT ATAAAAAAT AGMTAATTT AAAGGAAGTT GTCTGAACGG CAAAATTGAC							
2F melon genomic DNA							
-602	-592	-582	-572	-562	-552	-542	-532
*	*	*	*	*	*	*	*
AAAATATAC AAAGTTTAAAT GAACATGTGT CGAAATGTGT CGAAGAGGAA AGAAAACATT AAGTTTGAAA TATCTOGAGT							
2F melon genomic DNA							
-522	-512	-502	-492	-482	-472	-462	-452
*	*	*	*	*	*	*	*
TAAATACATA TCAATCCATA GTATATATATA ACAAAACAAA CTTAAATCTG AAAAAAAT TGAATTTAAT AAGAAAAAGA							
2F melon genomic DNA							
-442	-432	-422	-412	-402	-392	-382	-372
*	*	*	*	*	*	*	*
GATCAAACTC TTAATTTTTT AAAAAATAA TGGTGAAGAA AACTGAAAT TTTCATATAT TGTTTAATTT CAAATGATC							
2F melon genomic DNA							
-362	-352	-342	-332	-322	-312	-302	-292
*	*	*	*	*	*	*	*
CAAAAATPAA AGTTAAAAAA GCATTAAACA AAACAATICA AAACTAGCT ACTACACATT TACGAAAAATA TATGATACAC							
2F melon genomic DNA							
-282	-272	-262	-252	-242	-232	-222	-212
*	*	*	*	*	*	*	*
AAAGGATTTT TGGGTGTAAA CATCTTTTTT ATTTTATATA CACCAACTT CGTATATATT CACACATAAA GAAGGAAAAA							
2F melon genomic DNA							
-202	-192	-182	-172	-162	-152	-142	-132
*	*	*	*	*	*	*	*
GAATTAATGC AAGGGTGTG CCAATTACGT ACCGTGTGTA TATCTACTC ATCCGTTAGG TTCTCAATC TCCTCTCTC							
2F melon genomic DNA							
-122	-112	-102	-92	-82	-72	-62	-52
*	*	*	*	*	*	*	*
CCTGCTCTC TAAITATTTC TGCCAGCGAC CATATTTCAT TTTCATTTGT GTTGTTAAAA AGCCGAGAAT CGCAATCCTT							
2F melon genomic DNA							
-42	-32	-22	-12	-2	Translational start site		
*	*	*	*	*			
TTTCTCTCAC TCTTAATICA TTTCAMTIC ACAAAAAA A G GATCGGCAC CATGG							
					-BamHI- -NcoI-		
2F melon genomic DNA							

**Fig. 7C**





**Fig. 8**